



## Microbiological and Immunological Alterations Associated with Occupational Exposure Among Meat Production Workers

Nizom Ermatov<sup>1</sup>, Dilshod Alimukhamedov<sup>2</sup>, Kamol Ibrohimov<sup>3\*</sup>, Ilxom Shovaliyev<sup>4</sup>, Yulduz Musayeva<sup>5</sup>, Mafura Sagdullayeva<sup>6</sup>, Zebo Tadjieva<sup>7</sup>, Eldor Bo 'riboev<sup>8</sup>

<sup>1</sup>Doctor of Medical Sciences, Professor, Head of the Department of Hygiene of Children, Adolescents and Nutrition, Tashkent State Medical University, Tashkent, Uzbekistan.

<sup>2</sup>Professor, Doctor of Medical Sciences, Department of Hygiene of Children, Adolescents and Nutrition, Tashkent State Medical University, Tashkent, Uzbekistan.

<sup>3</sup>PhD, Department of Hygiene, Bukhara State Medical Institute named after Abu Ali ibn Sino, Bukhara, Uzbekistan.

<sup>4</sup>DSc, Associate Professor, Department of Hygiene of Children, Adolescents and Nutrition, Tashkent State Medical University, Tashkent, Uzbekistan.

<sup>5</sup>Professor, Department of Neurology and Medical Psychology, Tashkent State Medical University, Tashkent, Uzbekistan.

<sup>6</sup>PhD, Associate Professor, Department of Pediatrics No. 1, Tashkent State Medical University, Tashkent, Uzbekistan.

<sup>7</sup>PhD, Associate Professor, Head of the Department of Pediatrics and Higher Nursing Education, Khorezm State Medical Institute, Khorezm, Uzbekistan.

<sup>8</sup>PhD, Associate Professor, Department of Hygiene of Children, Adolescents and Nutrition, Tashkent State Medical University, Tashkent, Uzbekistan.

### Abstract

**Introduction.** The work environment in meat-production enterprises is characterized by regular occupational exposure to microorganisms, organic aerosols, and other biological factors. Long-term occupational exposure may lead to alterations in the upper respiratory tract microbiota, increased colonization by opportunistic microorganisms, and changes in immunological reactivity. This study aimed to comprehensively assess alterations in the upper respiratory tract microbiological profile and immunological parameters among workers employed in meat-production enterprises.

**Materials and Methods.** The study included workers employed in livestock farming, poultry farming, horse breeding, and sausage production. Microbiological examination of biological samples collected from the upper respiratory tract was performed to determine the species composition and frequency of detected microorganisms. Immunological status was assessed by measuring serum concentrations of IgM, IgG, IgE, IL-4, IL-6, and procalcitonin. The obtained parameters were compared with those of a control group and statistically analyzed according to production sector.

**Results.** In 70.0% of the examined workers, pathogenic and opportunistic microorganisms were detected alongside the normal upper respiratory tract microbiota. *Candida spp.* were detected in 44.4% of workers, *Staphylococcus aureus* in 38.9%, and *Escherichia coli* in 37.8%. Immunological assessment revealed production sector-specific alterations in humoral immune parameters and inflammatory mediators. Compared with the control group, IL-6 levels were approximately 6.0-fold higher in livestock workers, 4.6-fold higher in poultry workers, 4.3-fold higher in horse-breeding workers, and 3.8-fold higher in sausage-production workers. Significant alterations in IgM, IgG, IgE, IL-4, and procalcitonin levels were also observed compared with controls.

**Conclusion.** Alterations in the upper respiratory tract microbiota among meat-production workers were accompanied by changes in humoral immune responses and activation of inflammatory mediators. The integrated assessment of microbiological and immunological parameters may be valuable for identifying early biological effects associated with occupational exposure and for improving preventive measures in occupational health.

**Keywords:**

*Meat production, occupational exposure, microbiota, opportunistic microorganisms, immunoglobulins, cytokines, IL-6, procalcitonin.*

Available online: 01/09/2026

---

## Introduction

Meat production is an occupational environment in which workers are continuously exposed to biological materials originating from animals, carcasses, raw meat, organic residues, processing equipment, and contaminated surfaces. The interaction of these sources creates a complex microbial environment within slaughterhouses and meat-processing facilities, where microorganisms may circulate between animals, products, workers, equipment, and the surrounding environment. Studies characterizing meat-processing microbiomes have demonstrated that production facilities can harbor diverse and persistent bacterial communities, while technological operations and cross-contamination contribute to their distribution throughout the processing chain (Zwirzitz et al., 2020; Barcenilla et al., 2024; Xu et al., 2025). The composition of these microbial communities may also vary according to production practices, environmental conditions, sanitation procedures, and characteristics of the processed raw materials (Moradi et al., 2024).

Airborne biological contamination represents an important route of occupational exposure in these environments. Animal handling, slaughtering, evisceration, carcass processing, cutting, cleaning, and movement of organic materials can release bacteria, fungi, microbial fragments, endotoxin-containing particles, and organic dust into workplace air. Fungal contamination has been documented in slaughterhouse environments, including potentially relevant moulds and yeasts in workplace air and on occupational surfaces (Viegas et al., 2016; Rodrigues et al., 2025). Repeated inhalation of biologically active aerosols may adversely affect respiratory health, particularly when exposure occurs throughout the working day and over prolonged periods. Studies among slaughterhouse and poultry workers have reported respiratory symptoms and functional changes associated with occupational exposure to organic aerosols and related contaminants (Kasaeinasab et al., 2016; Donham et al., 2000; Taluja et al., 2018). The upper respiratory tract (URT) is one of the first biological barriers encountered by airborne microorganisms and therefore represents an important site for assessing occupational microbial exposure. Continuous contact with animal-derived microorganisms may alter resident microbial communities and facilitate transient or persistent colonization by opportunistic and potentially pathogenic species. This is particularly relevant in meat production, where close contact with animals and raw biological materials creates repeated opportunities for microbial transfer. Studies among beef-processing and livestock workers have demonstrated nasal carriage of *Staphylococcus aureus*, including livestock-associated and antimicrobial-resistant strains (Leibler et al., 2016; Nadimpalli et al., 2016). These findings suggest that the microbiological status of the URT may provide valuable information on the biological burden experienced by occupationally exposed workers.

Microbial colonization, however, represents only one component of the biological response to occupational exposure. Persistent exposure to microbial antigens, organic dust, and other biologically active agents may activate mucosal and systemic immune mechanisms, resulting in alterations in inflammatory and humoral responses. Experimental evidence from poultry environments has shown that repeated exposure to poultry-barn air and lipopolysaccharide can enhance inflammatory signaling pathways, supporting the biological plausibility of immune activation following repeated occupational exposure (Kaur & Sethi, 2019). Studies among slaughterhouse workers have also reported alterations in inflammatory biomarkers, including IL-6, together with impaired ventilatory function (Ramadan et al., 2024). Thus, the biological effects of occupational exposure in meat-production environments may extend beyond local microbial colonization and involve systemic immune-inflammatory responses.

The combined assessment of microbiological and immunological indicators may provide a more comprehensive characterization of occupational biological effects than either approach alone. IgM and IgG represent major components of humoral immune activity, whereas IgE is associated with sensitization and hypersensitivity responses. IL-4 and IL-6 participate in the regulation of immune and inflammatory pathways, while procalcitonin may provide complementary information regarding systemic inflammatory activity. However, previous research in meat-production environments has largely examined environmental microbial contamination, respiratory symptoms, pulmonary function, microbial carriage, or inflammatory indicators separately. Consequently, evidence regarding the coexistence of alterations in URT microbial profiles and systemic humoral and inflammatory biomarkers within the same occupational population remains limited.

An additional consideration is the heterogeneity of biological exposure across meat-production sectors. Livestock farming, poultry farming, horse breeding, and sausage production involve different animal species, raw materials, technological operations, environmental conditions, and degrees of direct contact with biological substrates. Therefore, treating meat-production workers as a single occupationally exposed population may obscure important sector-specific differences. Comparative evaluation across production sectors is necessary to identify groups with more pronounced microbiological and immunological alterations and to provide evidence for targeted occupational health surveillance and preventive strategies.

Accordingly, the present study aimed to comprehensively assess microbiological and immunological alterations among meat-production workers by characterizing the upper respiratory tract microbiota and evaluating serum IgM, IgG, IgE, IL-4, IL-6, and procalcitonin levels in comparison with a control group, while determining differences in biological responses across major meat-production sectors.

## Materials and Methods

### *Study Design and Participants*

A cross-sectional comparative study was conducted among workers employed in four meat-production sectors: livestock farming, poultry farming, horse breeding, and sausage production. The microbiological assessment included 90 occupationally exposed workers. Participants were grouped according to their primary production sector, and a non-occupationally exposed control group was included for comparison. The study design and selection of occupational groups were based on differences in exposure to animal-derived biological materials and microbial contamination of the working environment (Masyagutova & Bakirov, 2019).

### *Microbiological Assessment*

Upper respiratory tract samples were collected under aseptic conditions and examined using conventional culture-based bacteriological and mycological methods. Isolated microorganisms were identified according to their cultural, morphological, and biochemical characteristics. The analysis included *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Streptococcus spp.*, *Escherichia coli*, and *Candida spp.* Microbial abundance was expressed as lg CFU/mL, and the frequency of detection was calculated as the number and percentage of positive samples.

Workplace air was additionally assessed for total microbial count, staphylococci, enterobacteria, and fungi. Air samples were collected in the morning, at midday, and at the end of the work shift, and microbial concentrations were expressed as CFU/m<sup>3</sup>. Quantitative assessment of viable microorganisms in workplace air was performed according to established occupational microbiological approaches (van Cleef et al., 2011).

### Immunological Assessment

Peripheral venous blood samples were collected from participants, and serum was used for immunological analyses. Serum concentrations of IgM, IgG, IgE, IL-4, IL-6, and procalcitonin were determined using validated immunological assay procedures. The obtained values were compared between the occupational groups and the control group to assess sector-specific differences in humoral and inflammatory responses (Masyagutova & Bakirov, 2019).

### Statistical Analysis

Continuous variables were presented as mean  $\pm$  standard error ( $M \pm SEM$ ), and categorical variables as numbers and percentages. Comparisons were performed between occupational groups and controls and among the four production sectors. Categorical variables were analyzed using the  $\chi^2$  test or Fisher's exact test where appropriate. For quantitative variables, appropriate parametric or non-parametric tests were applied according to data distribution. Statistical significance was set at  $p < 0.05$ . Statistical results were reported according to recommendations for biomedical research (Lang & Altman, 2015).

### Ethics Statement

The study was approved by the Ethics Committee of Bukhara State Medical Institute, Bukhara, Uzbekistan, and conducted in accordance with local legislation, institutional requirements, and the principles of the Declaration of Helsinki. All participants provided written informed consent before participation.

### Results

Microbiological examination of the upper respiratory tract demonstrated clear differences in microbial composition and colonization levels among workers from different meat-production sectors. Resident microorganisms, primarily *Staphylococcus epidermidis* and *Streptococcus spp.*, predominated in all study groups; however, occupationally exposed workers showed a greater presence of opportunistic microorganisms compared with the control group. The highest *S. epidermidis* concentration was recorded among livestock workers ( $4.15 \pm 0.07$  lg CFU/mL), while *Streptococcus spp.* reached  $4.93 \pm 0.04$  lg CFU/mL in livestock workers and  $4.92 \pm 0.04$  lg CFU/mL in horse-breeding workers. Differences between the study groups were statistically significant for *S. epidermidis* ( $p < 0.05$ ) and *Streptococcus spp.* ( $p < 0.001$ ).

More pronounced differences were observed for opportunistic microorganisms. *Escherichia coli* showed the highest concentration among poultry workers ( $2.45 \pm 0.55$  lg CFU/mL), compared with  $0.19 \pm 0.13$  lg CFU/mL in the control group ( $p < 0.001$ ). Similarly, *Candida spp.* levels were highest among sausage-production ( $2.52 \pm 0.70$  lg CFU/mL) and poultry workers ( $2.38 \pm 0.54$  lg CFU/mL), whereas the corresponding value in controls was  $0.70 \pm 0.24$  lg CFU/mL ( $p < 0.01$ ). *Staphylococcus aureus* was also more abundant among poultry workers ( $2.25 \pm 0.62$  lg CFU/mL), although the overall between-group difference was not statistically significant ( $p > 0.05$ ). Thus, the microbiological profile varied according to production sector, with poultry and sausage-production workers showing the most pronounced colonization by opportunistic microorganisms (Table 1).

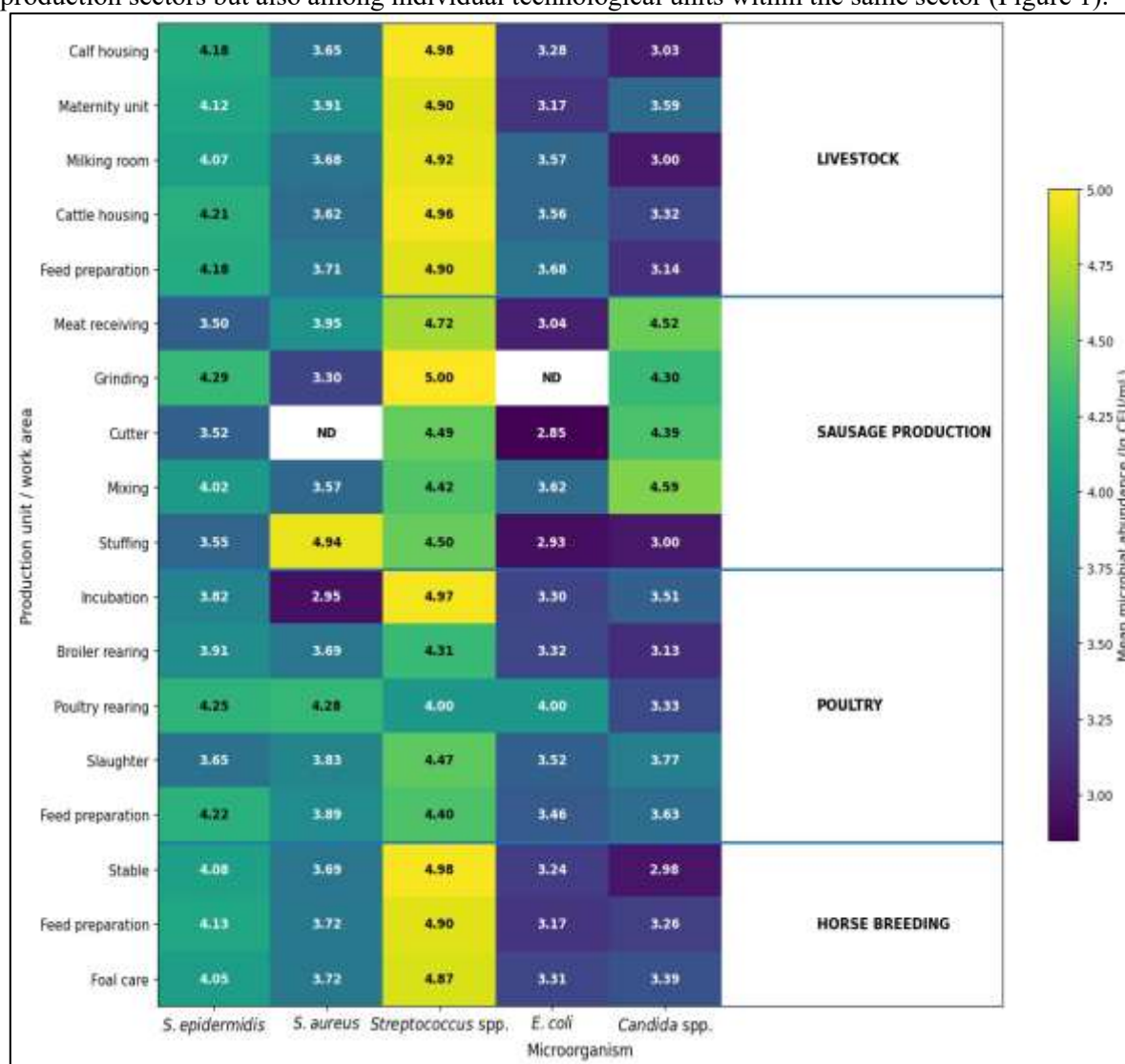
**Table 1. Microbiological Profile of the Upper Respiratory Tract in Meat-Production Workers by Occupational Sector**

| Microorganism                     | Sausage production | Poultry farming | Horse breeding  | Livestock farming | Control group   | p-value   |
|-----------------------------------|--------------------|-----------------|-----------------|-------------------|-----------------|-----------|
| <i>Staphylococcus epidermidis</i> | $3.77 \pm 0.13$    | $3.97 \pm 0.16$ | $4.09 \pm 0.08$ | $4.15 \pm 0.07$   | $3.89 \pm 0.06$ | $< 0.05$  |
| <i>Staphylococcus aureus</i>      | $1.58 \pm 0.66$    | $2.25 \pm 0.62$ | $1.24 \pm 0.33$ | $1.39 \pm 0.29$   | $0.78 \pm 0.26$ | $> 0.05$  |
| <i>Streptococcus spp.</i>         | $4.63 \pm 0.16$    | $4.43 \pm 0.12$ | $4.92 \pm 0.04$ | $4.93 \pm 0.04$   | $4.81 \pm 0.02$ | $< 0.001$ |
| <i>Escherichia coli</i>           | $1.53 \pm 0.52$    | $2.45 \pm 0.55$ | $0.87 \pm 0.27$ | $1.22 \pm 0.27$   | $0.19 \pm 0.13$ | $< 0.001$ |
| <i>Candida spp.</i>               | $2.52 \pm 0.70$    | $2.38 \pm 0.54$ | $1.18 \pm 0.29$ | $1.28 \pm 0.25$   | $0.70 \pm 0.24$ | $< 0.01$  |

As shown in Table 1, the upper respiratory tract microbiological profile differed across occupational groups. The most pronounced changes were observed for *Escherichia coli* and *Candida spp.*, with the

highest *E. coli* level detected among poultry workers ( $2.45 \pm 0.55$  lg CFU/mL) and the highest *Candida spp.* level among sausage-production workers ( $2.52 \pm 0.70$  lg CFU/mL). Significant between-group differences were found for *S. epidermidis* ( $p < 0.05$ ), *Streptococcus spp.* ( $p < 0.001$ ), *E. coli* ( $p < 0.001$ ), and *Candida spp.* ( $p < 0.01$ ), whereas differences in *S. aureus* did not reach statistical significance ( $p > 0.05$ ). Overall, opportunistic microbial colonization was more pronounced among poultry and sausage-production workers compared with the control group.

A detailed analysis of microbial abundance across individual production units revealed considerable variation in the upper respiratory tract microbiological profile of workers. *Streptococcus spp.* remained consistently abundant across most work areas, whereas *S. aureus*, *E. coli*, and *Candida spp.* showed greater sector- and workplace-specific variability. Particularly high *Candida spp.* levels were observed in several sausage-production units, while elevated *E. coli* values were characteristic of poultry-rearing areas. These findings demonstrate that microbial colonization patterns varied not only between production sectors but also among individual technological units within the same sector (Figure 1).



**Figure 1. Distribution of upper respiratory tract microbial abundance across work areas of meat-production sectors (lg CFU/mL).**

As shown in Figure 1, the distribution of upper respiratory tract microorganisms varied considerably across production sectors and individual work areas. *Streptococcus spp.* showed consistently high abundance across most workplaces, reaching its maximum level in the grinding unit of sausage production (5.00 lg CFU/mL). Among opportunistic microorganisms, marked workplace-specific differences were observed for *S. aureus*, *E. coli*, and *Candida spp.* The highest *S. aureus* level was recorded in the sausage-stuffing unit (4.94 lg CFU/mL), while *E. coli* reached its maximum in the poultry-rearing unit (4.00 lg CFU/mL). *Candida spp.* was particularly abundant in sausage-production areas, with the highest level observed in the mixing unit (4.59 lg CFU/mL). Overall, the heatmap

demonstrates substantial heterogeneity in microbial colonization across technological units, with opportunistic microorganisms showing the most pronounced variation in poultry and sausage-production environments

Immunological assessment was performed to determine sector-specific variations in humoral immune and inflammatory responses among workers employed in livestock farming, poultry farming, horse breeding, and sausage production. Serum concentrations of IgM, IgG, IgE, IL-4, IL-6, and procalcitonin were evaluated, and the results were summarized using minimum and maximum values, mean  $\pm$  standard error ( $M \pm SEM$ ), and 95% confidence intervals (Table 2).

**Table 2. Immunological and Inflammatory Biomarkers Among Meat-Production Workers by Occupational Sector**

| Biomarker             | Occupational sector       | Min    | Max    | $M \pm SEM$       | 95% CI        |
|-----------------------|---------------------------|--------|--------|-------------------|---------------|
| IgM, г/л              | Livestock farming (n=40)  | 1.10   | 4.10   | $2.18 \pm 0.11$   | 1.95-2.41     |
|                       | Poultry farming (n=30)    | 2.20   | 7.40   | $3.96 \pm 0.24$   | 3.46-4.46     |
|                       | Horse breeding (n=10)     | 1.10   | 3.60   | $2.69 \pm 0.24$   | 2.16-3.22     |
|                       | Sausage production (n=10) | 0.70   | 2.80   | $1.86 \pm 0.22$   | 1.37-2.35     |
| IgG, г/л              | Livestock farming (n=40)  | 3.40   | 37.50  | $23.87 \pm 0.95$  | 21.96-25.79   |
|                       | Poultry farming (n=30)    | 10.20  | 23.30  | $16.55 \pm 0.67$  | 15.18-17.92   |
|                       | Horse breeding (n=10)     | 13.60  | 31.40  | $21.76 \pm 1.86$  | 17.56-25.96   |
|                       | Sausage production (n=10) | 17.50  | 35.60  | $25.91 \pm 1.84$  | 21.75-30.07   |
| IgE, нг/мл            | Livestock farming (n=40)  | 175.10 | 286.40 | $224.33 \pm 4.64$ | 214.95-233.71 |
|                       | Poultry farming (n=30)    | 265.20 | 353.60 | $311.98 \pm 3.75$ | 304.31-319.66 |
|                       | Horse breeding (n=10)     | 252.60 | 355.90 | $297.04 \pm 8.80$ | 277.14-316.94 |
|                       | Sausage production (n=10) | 287.20 | 346.40 | $313.59 \pm 6.79$ | 298.24-328.94 |
| IL-6, pg/ml           | Livestock farming (n=40)  | 21.00  | 45.40  | $34.45 \pm 1.23$  | 31.95-36.95   |
|                       | Poultry farming (n=30)    | 15.80  | 35.40  | $26.43 \pm 1.04$  | 24.30-28.56   |
|                       | Horse breeding (n=10)     | 12.50  | 32.10  | $24.92 \pm 1.95$  | 20.52-29.32   |
|                       | Sausage production (n=10) | 12.80  | 28.70  | $21.97 \pm 1.75$  | 18.00-25.94   |
| IL-4, pg/ml           | Livestock farming (n=40)  | 1.30   | 10.60  | $6.23 \pm 0.34$   | 5.54-6.92     |
|                       | Poultry farming (n=30)    | 2.20   | 12.40  | $6.95 \pm 0.58$   | 5.76-8.13     |
|                       | Horse breeding (n=10)     | 2.90   | 10.30  | $6.10 \pm 0.74$   | 4.43-7.77     |
|                       | Sausage production (n=10) | 2.60   | 9.60   | $4.99 \pm 0.75$   | 3.30-6.68     |
| Прокальцитонин, pg/ml | Livestock farming (n=40)  | 0.05   | 0.26   | $0.155 \pm 0.009$ | 0.137-0.173   |
|                       | Poultry farming (n=30)    | 0.01   | 0.09   | $0.057 \pm 0.005$ | 0.048-0.066   |

|  |                              |      |      |             |             |
|--|------------------------------|------|------|-------------|-------------|
|  | Horse breeding<br>(n=10)     | 0.08 | 0.15 | 0.115±0.008 | 0.096-0.134 |
|  | Sausage production<br>(n=10) | 0.11 | 0.19 | 0.149±0.009 | 0.129-0.169 |

The data presented in Table 2 demonstrated distinct variations in immunological and inflammatory parameters among workers across the different meat-production sectors. The highest IgM concentration was observed among poultry workers (3.96±0.24 g/L), whereas the highest IgG level was recorded among sausage-production workers (25.91±1.84 g/L). IgE concentrations were also notably high among sausage-production (313.59±6.79 ng/mL) and poultry workers (311.98±3.75 ng/mL).

Sector-specific differences were also evident in cytokine levels. The highest IL-6 concentration was observed among livestock workers (34.45±1.23 pg/mL), while IL-4 reached its highest level among poultry workers (6.95±0.58 pg/mL). Procalcitonin levels were highest in livestock (0.155±0.009 pg/mL) and sausage-production workers (0.149±0.009 pg/mL). Overall, the findings indicate heterogeneous, sector-specific patterns of humoral and inflammatory responses, with the most pronounced alterations observed among poultry, livestock, and sausage-production workers.

To assess the direction and magnitude of immunological alterations among workers across different meat-production sectors, serum levels of IgM, IgG, IgE, IL-4, IL-6, and procalcitonin were comparatively analyzed against those of the control group. This comparative analysis enabled the identification of sector-specific patterns of immune response and the extent to which immunological parameters differed from control values (Table 3).

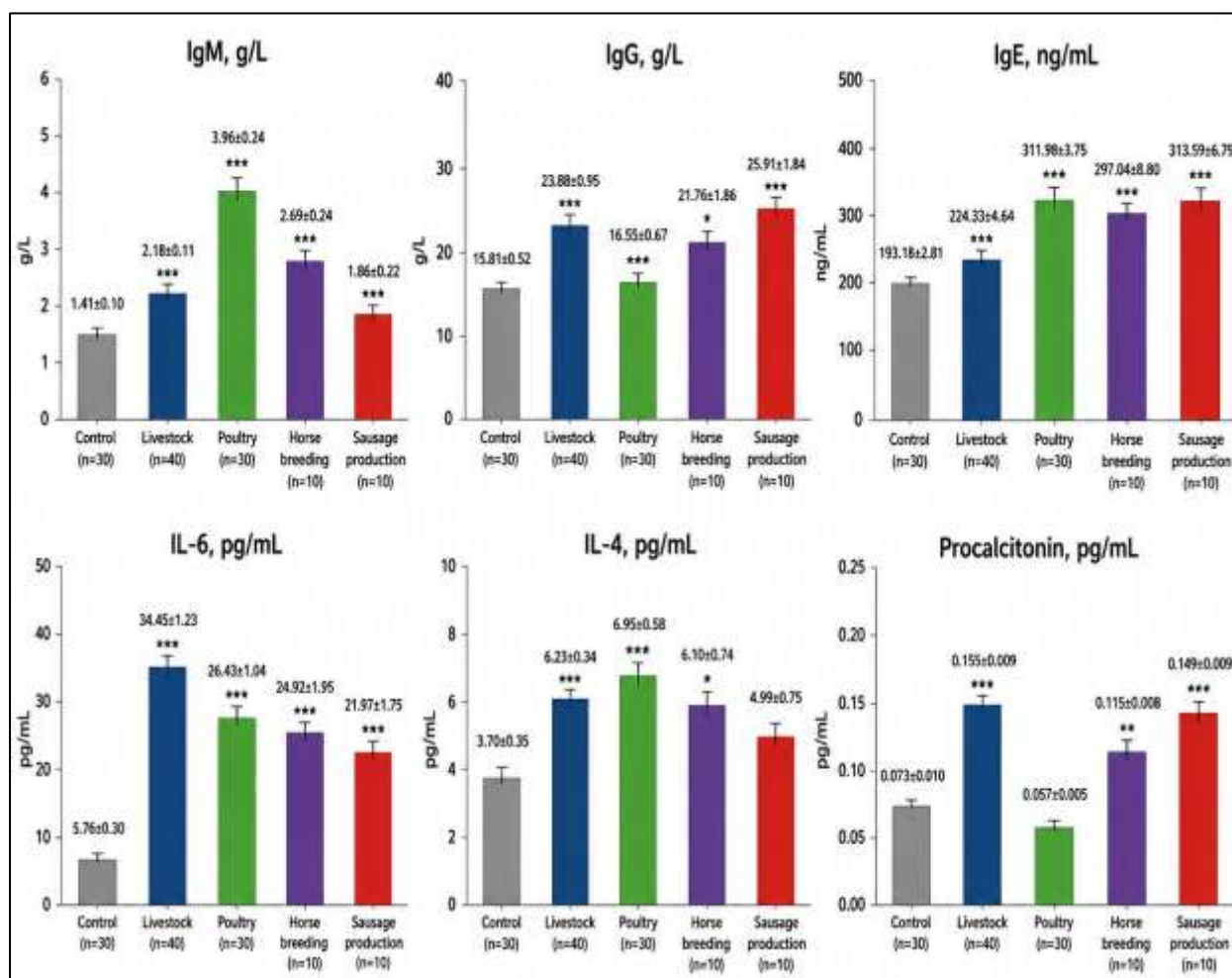
**Table 3. Comparison of Immunological and Inflammatory Biomarkers Between Meat-Production Workers and the Control Group**

| Study group               | IgM, g/L          | IgG, g/L           | IgE, ng/mL          | IL-6, pg/mL        | IL-4, pg/mL       | Procalcitonin, pg/mL |
|---------------------------|-------------------|--------------------|---------------------|--------------------|-------------------|----------------------|
| Control (n=30)            | 1,41±0,10         | 15,81±0,52         | 193,18±2,81         | 5,76±0,30          | 3,70±0,35         | 0,073±0,010          |
| Livestock (n=40)          | 2,18±0,11*<br>**↑ | 23,88±0,95<br>***↑ | 224,33±4,64<br>***↑ | 34,45±1,23*<br>**↑ | 6,23±0,34*<br>**↑ | 0,155±0,009***↑      |
| Poultry (n=30)            | 3,96±0,24*<br>**↑ | 16,55±0,67         | 311,98±3,75<br>***↑ | 26,43±1,04*<br>**↑ | 6,95±0,58*<br>**↑ | 0,057±0,005          |
| Horse breeding (n=10)     | 2,69±0,24*<br>**↑ | 21,76±1,86<br>*↑   | 297,04±8,80<br>***↑ | 24,92±1,95*<br>**↑ | 6,10±0,74*<br>↑   | 0,115±0,008***↑      |
| Sausage production (n=10) | 1,86±0,22         | 25,91±1,84<br>***↑ | 313,59±6,79<br>***↑ | 21,97±1,75*<br>**↑ | 4,99±0,75         | 0,149±0,009***↑      |

**Note:** Values are presented as M±SEM. Statistical significance compared with the control group: \*p<0.05; \*\*p<0.01; \*\*\*p<0.001. ↑ indicates an increase relative to the control group.

Comparative analysis with the control group demonstrated distinct sector-specific patterns of immunological response. The most pronounced alteration was observed in IL-6 levels, which were significantly elevated across all occupational groups compared with controls (p<0.001), with the highest concentration recorded among livestock workers (34.45±1.23 pg/mL). IgM reached its highest level among poultry workers (3.96±0.24 g/L; p<0.001), whereas the highest IgG concentration was observed in sausage-production workers (25.91±1.84 g/L; p<0.001). IgE levels were particularly elevated in the poultry and sausage-production groups, with both showing significant differences from the control group (p<0.001). IL-4 was significantly increased among livestock and poultry workers (p<0.001), while the highest procalcitonin levels were recorded in livestock and sausage-production workers (p<0.001). Overall, these findings demonstrate distinct occupational sector-specific profiles of immunological and inflammatory responses.

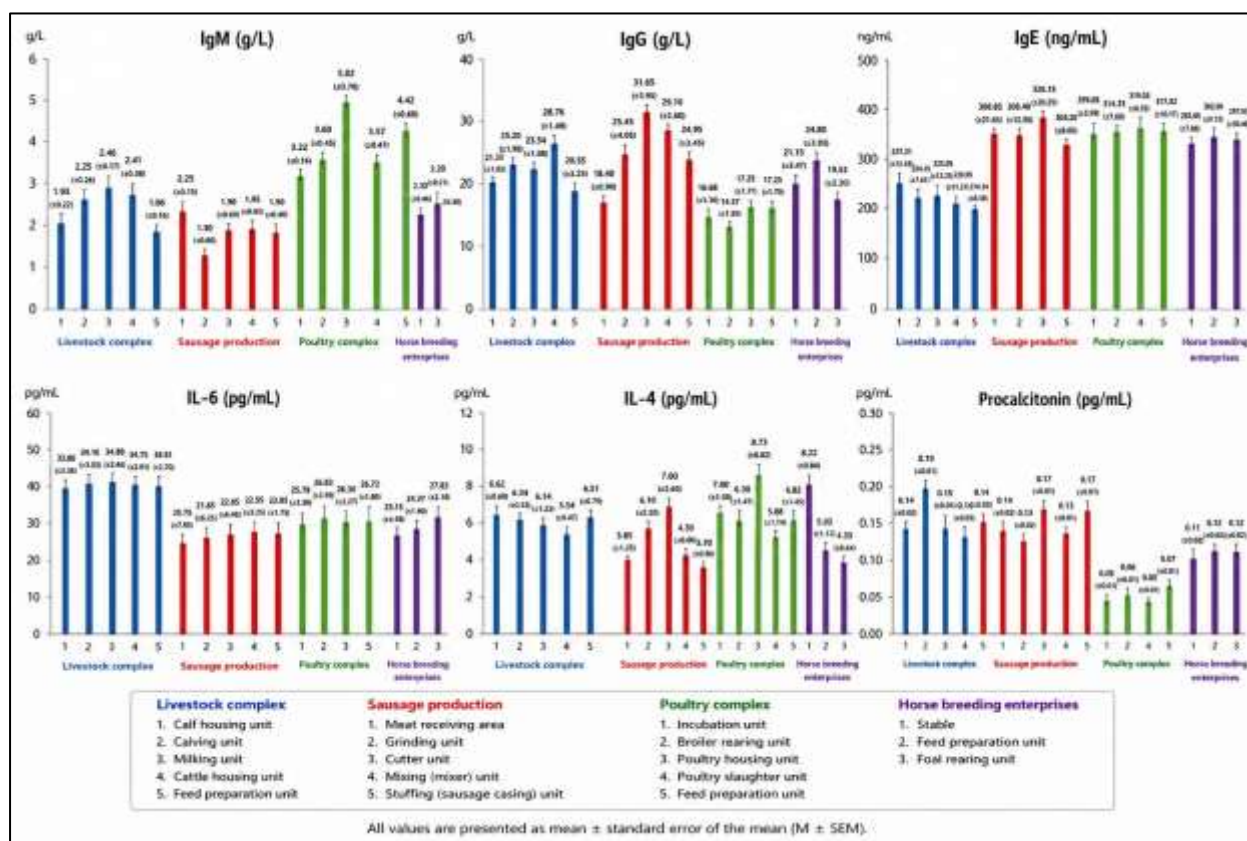
To visually assess sector-specific variations in immunological and inflammatory parameters, serum levels of IgM, IgG, IgE, IL-6, IL-4, and procalcitonin were graphically compared with those of the control group. The results are presented as mean ± standard error of the mean (M ± SEM) for each study group, with statistically significant differences relative to the control group indicated accordingly (Figure 2).



**Figure 2. Comparative Analysis of Immunological and Inflammatory Biomarkers Among Workers in Different Meat Production Sectors and the Control Group**

The comparative profile of immunological biomarkers revealed marked heterogeneity in the magnitude of response across occupational sectors. The most prominent finding was the consistently elevated IL-6 level in all exposed groups, with the greatest increase observed among livestock workers. Poultry workers exhibited a distinct response characterized by the highest IgM and IL-4 levels together with a pronounced elevation in IgE. In contrast, sausage-production workers showed the highest IgG and IgE concentrations and a substantial increase in procalcitonin. Horse-breeding workers demonstrated an intermediate response across most biomarkers. Notably, procalcitonin levels in poultry workers did not increase relative to the control group, indicating that the immunological response was not uniform across biomarkers or occupational settings. Collectively, these findings demonstrate distinct sector-specific immunological profiles, with IL-6 representing the most consistently altered inflammatory marker across the studied occupational groups.

To characterize workplace-specific variations in immunological responses, serum levels of IgM, IgG, IgE, IL-6, IL-4, and procalcitonin were compared across individual production units within the four occupational sectors. The biomarker profiles showed considerable variation between technological units, indicating a heterogeneous immunological response across different workplace environments. The most pronounced differences were observed for IgE, IL-6, and procalcitonin, whereas the magnitude and pattern of changes in IgM, IgG, and IL-4 varied according to both occupational sector and production unit. The unit-specific distributions of all investigated biomarkers, expressed as mean  $\pm$  SEM, are presented in Figure 3.



**Figure 3. Workplace-Specific Distribution of Immunological and Inflammatory Biomarkers Across Meat-Production Sectors**

Workplace-specific analysis revealed substantial heterogeneity in immunological and inflammatory biomarker profiles across individual production units. Within the livestock sector, IL-6 remained consistently elevated across all workplaces, reaching its highest level among workers in the milking unit ( $34.88 \pm 2.46$  pg/mL), whereas the highest IgG concentration was observed in the cattle-housing unit ( $28.76 \pm 1.49$  g/L). In sausage production, IgE levels were consistently high across production units, with the maximum value recorded in the cutter unit ( $326.15 \pm 20.25$  ng/mL), where relatively high levels of IgG and IL-4 were also observed.

In the poultry sector, the most pronounced biomarker profile was observed among workers in the poultry-rearing unit, which exhibited the highest IgM ( $5.02 \pm 0.70$  g/L), IgE ( $319.03 \pm 6.33$  ng/mL), and IL-4 ( $8.73 \pm 0.82$  pg/mL) levels within this sector. Among horse-breeding workers, the highest IgG concentration was recorded in the feed-preparation unit ( $24.80 \pm 3.93$  g/L), whereas IL-6 peaked among workers involved in foal care ( $27.83 \pm 2.18$  pg/mL), and IL-4 was highest among stable workers ( $8.22 \pm 0.84$  pg/mL). Overall, the workplace-level analysis demonstrated that the magnitude and pattern of immunological alterations varied not only between occupational sectors but also among individual technological units within the same sector.

## Discussion

The present findings demonstrate that occupational exposure in meat-production settings is associated with concurrent alterations in upper respiratory tract (URT) microbial colonization and systemic humoral and inflammatory responses, with the pattern and magnitude of these changes varying across production sectors and individual technological units. The increased detection of opportunistic microorganisms, particularly *Escherichia coli* and *Candida spp.*, together with sector-specific changes in IgM, IgG, IgE, IL-4, IL-6, and procalcitonin, suggests that biological exposure in meat-production environments is heterogeneous and may induce different patterns of immune response. Among the investigated biomarkers, IL-6 showed the most consistent alteration, with elevated concentrations across all occupational groups compared with the control group.

The shift toward greater abundance of opportunistic microorganisms among occupationally exposed workers is consistent with evidence that prolonged contact with livestock and animal-associated

environments may alter the composition of the upper respiratory tract microbiome. Studies of livestock workers have demonstrated differences in nasal and oropharyngeal microbial communities associated with occupational animal exposure (Kates et al., 2019). Furthermore, livestock-related environmental exposure has been associated with alterations in the oropharyngeal microbiome, supporting the concept that airborne biological agents originating from animal-production environments may influence respiratory microbial communities (Van Kersen et al., 2022). More recent evidence also indicates that occupational and environmental livestock exposures are associated with alterations in the upper respiratory tract microbiome (Hewitt et al., 2025). These observations provide an epidemiological context for the pronounced *E. coli* and *Candida spp.* colonization identified in the present study, particularly among poultry and sausage-production workers.

The systemic immunological findings are also consistent with the established biological effects of organic dust and bioaerosol exposure in agricultural occupations. Organic dust generated in animal-production environments contains a complex mixture of microbial components capable of activating inflammatory and immunological pathways following inhalation. Previous evidence has shown that agricultural organic dust exposure can induce both innate inflammatory and adaptive immune responses (Poole & Romberger, 2012). Experimental inhalation of swine dust has also been demonstrated to induce cytokine release in the upper and lower airways, providing biological evidence that exposure to animal-derived organic aerosols can initiate substantial inflammatory responses (Wang et al., 1997). These mechanisms may contribute to the pronounced inflammatory biomarker changes observed among occupationally exposed workers in the present study.

IL-6 was the most consistently altered immunological marker, being elevated across all four occupational sectors and reaching the highest concentration among livestock workers. This pattern may reflect sustained inflammatory activation associated with repeated contact with microbial antigens and biologically active components of organic aerosols. Importantly, recent findings among workers in agro-industrial enterprises have demonstrated that occupational bioaerosol exposure is accompanied by measurable immunological alterations, further supporting the relationship between biologically contaminated occupational environments and altered immune responses (Ibrokhimov et al., 2026). The present results extend this evidence by demonstrating that the magnitude of immune-inflammatory alterations differs not only between major production sectors but also between individual technological units within meat-production enterprises.

In contrast to the relatively consistent IL-6 response, humoral immune markers demonstrated pronounced sector-specific variation. Poultry workers exhibited the highest IgM concentration together with marked increases in IgE and IL-4, whereas sausage-production workers showed particularly high IgG and IgE concentrations. Livestock workers were characterized by pronounced IL-6 and procalcitonin levels. The concurrent increase in IgE and IL-4 among poultry workers may be compatible with enhanced type-2 immune activity or sensitization-related responses. However, allergen-specific IgE and clinical sensitization were not assessed in the present study; therefore, these findings should not be interpreted as direct evidence of occupational allergy. Rather, they demonstrate that different occupational environments are associated with distinct humoral and inflammatory profiles that warrant further investigation.

The combination of elevated IgM, IgE, and IL-4 with comparatively unchanged procalcitonin among poultry workers is particularly noteworthy. This pattern suggests that the immunological response in this group may differ from the more pronounced inflammatory profile observed among livestock workers. Procalcitonin is generally associated with systemic inflammatory responses, whereas IgE and IL-4 are more closely related to humoral and type-2 immune pathways. Consequently, the observed differences support the use of a multi-marker approach when investigating occupational biological exposure, as reliance on a single inflammatory biomarker may fail to characterize the diversity of biological responses across production environments. Nevertheless, the clinical relevance and occupational screening value of these biomarkers require confirmation in longitudinal studies.

Workplace-level analysis provided further evidence of heterogeneity within individual sectors. For example, IL-6 remained consistently high across livestock-production units, whereas poultry-rearing workers demonstrated particularly pronounced IgM, IgE, and IL-4 levels. In sausage production, IgE concentrations were elevated across several technological units, while horse-breeding workplaces showed a more variable immunological profile. These differences suggest that occupational biological exposure is determined not only by the general production sector but also by the specific tasks and technological operations performed by workers. Differences in animal contact, handling of biological

materials, organic aerosol generation, ventilation, sanitation, and duration of exposure may contribute to the observed workplace-specific patterns.

The simultaneous presence of altered URT microbial profiles and systemic immunological changes represents an important aspect of the present findings. Occupational microbiome studies have demonstrated that livestock-associated environmental exposures can modify respiratory microbial communities (Kates et al., 2019; Van Kersen et al., 2022; Hewitt et al., 2025), whereas research on agricultural organic dust has established its capacity to induce inflammatory responses (Poole & Romberger, 2012; Wang et al., 1997). The present study brings these two components together by evaluating microbiological colonization and systemic immunological biomarkers within the same occupational population. However, the coexistence of these alterations does not demonstrate that specific microorganisms directly caused individual immunological changes. Further studies incorporating individual exposure measurements and microbiological–immunological correlation analyses are required to clarify these relationships.

### Limitations

Several limitations should be considered when interpreting the results. First, the cross-sectional design does not allow determination of the temporal sequence or causality between occupational biological exposure, URT microbial colonization, and immunological alterations. Second, the relatively small sample sizes in the horse-breeding and sausage-production groups may reduce the statistical precision of comparisons involving these sectors. Third, culture-based microbiological methods primarily detect viable cultivable microorganisms and may therefore underestimate the overall diversity of the respiratory microbiota. Molecular and sequencing-based approaches could provide a more comprehensive characterization in future investigations. In addition, potential individual-level confounding factors, including smoking, atopic predisposition, previous respiratory disease, medication use, and duration of occupational exposure, should be considered in subsequent studies.

### Practical Implications

The sector- and workplace-specific microbiological and immunological profiles observed in this study support a targeted approach to biological risk assessment in meat-production enterprises. Recent evidence that occupational bioaerosol exposure among agro-industrial workers is associated with immunological changes further emphasizes the importance of integrating exposure assessment with worker health surveillance (Ibrokhimov et al., 2026). Preventive strategies should prioritize technological units with substantial biological exposure and include effective ventilation, control of organic dust and bioaerosols, adequate workplace sanitation, and appropriate respiratory protective equipment.

The combined evaluation of microbiological and immunological parameters may also provide additional information for identifying groups potentially experiencing greater biological exposure. However, IL-6, immunoglobulins, IL-4, and procalcitonin should not yet be considered established routine occupational screening biomarkers based on the present cross-sectional findings alone. Longitudinal studies incorporating quantitative bioaerosol and endotoxin measurements, molecular characterization of respiratory microbial communities, and repeated immunological assessments are required to determine their predictive and preventive value. Such an integrated approach may contribute to more precise identification of biological hazards and the development of task-specific preventive strategies in meat-production workplaces.

### Conclusion

This study demonstrates that occupational exposure in meat-production enterprises is associated with concurrent alterations in upper respiratory tract microbial colonization and systemic immunological reactivity, with the pattern and magnitude of these changes varying according to production sector. Increased colonization by opportunistic microorganisms, particularly *Candida* spp., *Staphylococcus aureus*, and *Escherichia coli*, was accompanied by significant elevations in IgM, IgG, IgE, IL-4, IL-6, and procalcitonin relative to the control group, with IL-6 representing the most consistently altered biomarker across all occupational groups. These findings indicate that the combined assessment of microbiological and immunological parameters provides a more informative picture of occupational biological burden than either approach applied separately, and may serve as a basis for developing

sector- and task-specific preventive measures, enhanced workplace hygiene, and targeted health-monitoring programs for workers in meat-production enterprises.

### Acknowledgments

The authors are grateful to the staff of the Department of Occupational Hygiene and the Scientific Committee of Bukhara State Medical Institute, Bukhara, Uzbekistan, for their support and assistance during the conduct of this study.

### Novelty statement

Using an integrated microbiological and immunological approach, this study reveals sector- and workplace-specific patterns of upper respiratory tract microbial colonization and humoral/inflammatory response among workers employed in livestock farming, poultry farming, horse breeding, and sausage production, providing new evidence to support targeted occupational health surveillance in the meat-production industry.

### Author's contribution

All authors contributed equally to this work.

### Conflict of Interest

The authors state that they have no conflicts of interest.

### References

1. Barcenilla, C., Cobo-Díaz, J. F., Puente, A., Valentino, V., De Filippis, F., Ercolini, D., Carlino, N., Pinto, F., Segata, N., Prieto, M., López, M., & Alvarez-Ordóñez, A. (2024). In-depth characterization of food and environmental microbiomes across different meat processing plants. *Microbiome*, 12(1), 199. <https://doi.org/10.1186/s40168-024-01856-3>
2. Donham, K. J., Cumro, D., Reynolds, S. J., & Merchant, J. A. (2000). Dose-Response relationships between occupational aerosol exposures and Cross-Shift declines of lung function in poultry workers: *Journal of Occupational and Environmental Medicine*, 42(3), 260–269. <https://doi.org/10.1097/00043764-200003000-00006>
3. Kasaeinasab, A., Jahangiri, M., Karimi, A., Tabatabaei, H. R., & Safari, S. (2016). Respiratory disorders among workers in slaughterhouses. *Safety and Health at Work*, 8(1), 84–88. <https://doi.org/10.1016/j.shaw.2016.04.002>
4. Kaur, G., & Sethi, R. S. (2019). Multiple exposures to poultry barn air and lipopolysaccharide synergistically increase the pulmonary expression of TLR-4 and IL-1 $\beta$ . *Journal of Occupational Health*, 62(1), e12094. <https://doi.org/10.1002/1348-9585.12094>
5. Leibler, J. H., Jordan, J. A., Brownstein, K., Lander, L., Price, L. B., & Perry, M. J. (2016). Staphylococcus aureus Nasal Carriage among Beefpacking Workers in a Midwestern United States Slaughterhouse. *PLoS ONE*, 11(2), e0148789. <https://doi.org/10.1371/journal.pone.0148789>
6. ManpreetKaurTaluja, M., VidushiGupta, V., GarimaSharma, G., & JaspreetSinghArora, J. (2018). PREVALENCE OF SYMPTOMS (RESPIRATORY AND NON-RESPIRATORY) AMONG POULTRY FARM WORKERS IN INDIA. *American Journal of Physiology Biochemistry and Pharmacology*, 8(2), 40. <https://doi.org/10.5455/ajpbp.20180913111012>
7. Nadimpalli, M., Stewart, J. R., Pierce, E., Pisanic, N., Love, D. C., Hall, D., Larsen, J., Carroll, K. C., Tekle, T., Perl, T. M., & Heaney, C. D. (2016). Livestock-Associated, Antibiotic-Resistant Staphylococcus aureus Nasal Carriage and Recent Skin and Soft Tissue Infection among Industrial Hog Operation Workers. *PLoS ONE*, 11(11), e0165713. <https://doi.org/10.1371/journal.pone.0165713>
8. Ramadan, M. A., Mohammed, R. S., & Eldin, A. S. S. (2024). Assessment of ventilatory functions and associated inflammatory markers among workers in slaughterhouses. *International Archives of Occupational and Environmental Health*, 97(8), 891–900. <https://doi.org/10.1007/s00420-024-02094-8>
9. Rodrigues, M. A., Teiga-Teixeira, P., & Esteves, A. (2025). Occurrence of moulds and yeasts in the slaughterhouse: The underestimated role of fungi in meat safety and occupational health. *Foods*, 14(8), 1320. <https://doi.org/10.3390/foods14081320>
10. Viegas, C., Faria, T., Santos, M. D., Carolino, E., Sabino, R., Gomes, A. Q., & Viegas, S. (2016). Slaughterhouses Fungal Burden Assessment: A contribution for the pursuit of a better assessment strategy. *International Journal of Environmental Research and Public Health*, 13(3), 297.

<https://doi.org/10.3390/ijerph13030297>

11. Xu, Z. S., Pham, V. D., Yang, X., & Gänzle, M. G. (2025). High-throughput analysis of microbiomes in a meat processing facility: are food processing facilities an establishment niche for persisting bacterial communities? *Microbiome*, 13(1), 25. <https://doi.org/10.1186/s40168-024-02026-1>

12. Yang, X., Narvaez-Bravo, C., & Zhang, P. (2024). Driving forces shaping the microbial ecology in meat packing plants. *Frontiers in Microbiology*, 14, 1333696.

<https://doi.org/10.3389/fmicb.2023.1333696>

13. Zwirzitz, B., Wetzels, S. U., Dixon, E. D., Stessl, B., Zaiser, A., Rabanser, I., Thalgut, S., Pinior, B., Roch, F., Strachan, C., Zanghellini, J., Dzieciol, M., Wagner, M., & Selberherr, E. (2020). The sources and transmission routes of microbial populations throughout a meat processing facility. *Npj Biofilms and Microbiomes*, 6(1), 26. <https://doi.org/10.1038/s41522-020-0136-z>

14. Masyagutova, L. M., & Bakirov, A. B. (2019). Immunological indices in workers of various livestock productions. *Hygiene and Sanitation*, 98(9), 972–977. <https://doi.org/10.18821/0016-9900-2019-98-9-972-977>

15. Van Cleef, B. a. G. L., Graveland, H., Haenen, A. P. J., Van De Giessen, A. W., Heederik, D., Wagenaar, J. A., & Kluytmans, J. a. J. W. (2011). Persistence of Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* in Field Workers after Short-Term Occupational Exposure to Pigs and Veal Calves. *Journal of Clinical Microbiology*, 49(3), 1030–1033.

<https://doi.org/10.1128/jcm.00493-10>

16. Van Cleef, B. A., Verkade, E. J. M., Wulf, M. W., Buiting, A. G., Voss, A., Huijsdens, X. W., Van Pelt, W., Mulders, M. N., & Kluytmans, J. A. (2010). Prevalence of Livestock-Associated MRSA in Communities with High Pig-Densities in The Netherlands. *PLoS ONE*, 5(2), e9385.

<https://doi.org/10.1371/journal.pone.0009385>

17. Lang, T. A., & Altman, D. G. (2014). Basic statistical reporting for articles published in Biomedical Journals: The “Statistical Analyses and Methods in the Published Literature” or the SAMPL Guidelines. *International Journal of Nursing Studies*, 52(1), 5–9. <https://doi.org/10.1016/j.ijnurstu.2014.09.006>

18. Ibrokhimov K.I., Iskandarova G.T., Ermatov N.J., Abdurakhimov B., Nasirdinov M. Occupational exposure of bioaerosols to workers of agro-industrial enterprises and related immunological changes. *Russian Journal of Occupational Health and Industrial Ecology*. 2026;66(6):414-422. (In Russ.) <https://doi.org/10.31089/1026-9428-2026-66-6-414-422>.

19. Hewitt, B. C., Odendaal, M., De Rooij, M. M., Bossers, A., Chu, M. L., Van Kersen, W., Lotterman, A., Van Der Giessen, J., Bogaert, D., & Smit, L. A. (2025). Occupational and environmental livestock exposures are associated with alterations in the upper respiratory tract microbiome. *Environmental Research*, 286(Pt 1), 122847. <https://doi.org/10.1016/j.envres.2025.122847>

20. Kates, A. E., Dalman, M., Torner, J. C., & Smith, T. C. (2019). The nasal and oropharyngeal microbiomes of healthy livestock workers. *PLoS ONE*, 14(3), e0212949.

<https://doi.org/10.1371/journal.pone.0212949>

21. Poole, J. A., & Romberger, D. J. (2012). Immunological and inflammatory responses to organic dust in agriculture. *Current Opinion in Allergy and Clinical Immunology*, 12(2), 126–132.

<https://doi.org/10.1097/aci.0b013e3283511d0e>

22. Van Kersen, W., Bossers, A., De Steenhuijsen Piters, W. A., De Rooij, M. M., Bonten, M., Fluit, A. C., Heederik, D., Paganelli, F. L., Rogers, M., Viveen, M., Bogaert, D., Leavis, H. L., & Smit, L. A. (2022). Air pollution from livestock farms and the oropharyngeal microbiome of COPD patients and controls. *Environment International*, 169, 107497. <https://doi.org/10.1016/j.envint.2022.107497>

23. Wang, Z., Larsson, K., Palmberg, L., Malmberg, P., Larsson, P., & Larsson, L. (1997). Inhalation of swine dust induces cytokine release in the upper and lower airways. *European Respiratory Journal*, 10(2), 381–387. <https://doi.org/10.1183/09031936.97.10020381>

24. Ibrokhimov K.I., Iskandarova G.T., Ermatov N.J., Abdurakhimov B., Nasirdinov M. Occupational exposure of bioaerosols to workers of agro-industrial enterprises and related immunological changes. *Russian Journal of Occupational Health and Industrial Ecology*. 2026;66(6):414-422. (In Russ.) <https://doi.org/10.31089/1026-9428-2026-66-6-414-422>.